



hDEC2a

DEC1

MDEGIPHLQERQ—L——LEHRDFIGLDYSSLYMC-KPKRSMKRD-DTKDITYKLPHRLIEKKRRDRIN 61
M-ERIPSAQPPACLPKAPGLEHGDLPGMYPAMHYQVYKSRRGIKRSSEDSKETYKLPHRLIEKKRRDRIN 69

ECIAQLKOLLPEHLKLTTLGHLEKAVVLELTLKHLKALTALTEQQHQKIIALQNG——ERSLKSPIQSD 127
ECIAQLKOLLPEHLKLTTLGHLEKAVVLELTLKHVKALTNLIDQQQKIIALQSGLOAGELSGR-NVETG 138

LDAFHSGFQTCAKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGA---PS 194
QEMFCSGFQTCAREVLQYLAKHEN-T-RDLKSSQLVTHLHRVVSELLQGGTSRKPSDPAPKVMDFKEKPS 206

A-A-GSAAAPCLERAGQKLEPLAYCVPVIQRTQP-SAEIAAENDTDTDSGYGGAEARPD-R-E——K- 254
SPAKGSEG-P——G-K--N—CVPVIQRTFAHSSGEQSGSDTDTDSGYGGESEKG-DLRSEQPCFKS 263

—GK—GAGASRVTIKQEPAGEDSPAPK-RMKL-DSRGGG-SGGGPGGGAAAAAALLGPDAAAAALLR 317
DHGRRTMGERIGAIIKQESE-E-PPTKKNRMQLSDDEGHFTSS—————D————— 305

PDAALLSSLVAFGGGGGAPFP-QPAAAAAPFCLPFCFLSP-SAAAAYVQPFLLDKSGLEKYLPAAAAAAPF 385
——LISS—PFLG——PHPHQP——PFCLPF-YLIPPSATA-YL-PML——EKCWYPTSV—P- 349

PLLYPGIPAPAAAAAAAAAAAAAAAAAFPCSSVLSPPPEKAGAAAATLL-PHEVAPLGAPHPQHPHGRTH 454
VL-YPGLNASAAA—————LSSFMNP-DKISA—PLLMPQR—L—PSP————— 385

LPFAGPREPGNPRESSA—QE-DPSQPGK-EA-P 482
LP-AHP——SVDSSVLLQALKPIPLNLETKD

(Homology 43%)

FIG. 1



hDEC2a

hDEC2b

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTK--DTYKLPRLIEKKRRDRINECIAQLK 68

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKVSDTYKLPRLIEKKRRDRINECIAQLK 70

DLLPEHLKLTTLGHLEKAVVLELT LKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTC 138

DLLPEHLKLTTLGHLEKAVVLELT LKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTC 140

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 208

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 210

OKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGGEAEARP DREKKGAGASRVTIKQEPPEGEDSPAPK 278

OKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGGEAEARP DREKKGAGASRVTIKQEPPEGEDSPAPK 280

RMKLDSRGGSGGGPGGGAAAAAALLGPDPAALLLRPDAALLSSLVAFGGGGGAPFPQAAAAAPFC 348

RMKLDSRGGSGGGPGGGAAAAAALLGPDPAALLLRPDAALLSSLVAFGGGGGAPFPQAAAAAPFC 350

LPFCFLSPSAAAAYVQPF LDKSGLEKYLPAALAAAPFLLYPGIPAPAAAAAAAAAAAAAFPC LSSV 418

LPFCFLSPSAAAAYVQPF LDKSGLEKYLPAALAAAPFLLYPGIPAPAAAAAAAAAAAAAFPC LSSV 420

LSPPPEKAGAAAATLLPHEVAPLGAPHPQHHPGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 482

LSPPPEKAGAAAATLLPHEVAPLGAPHPQHHPGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 484

FIG. 2

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hDEC2a

mDEC2a

MDEGIPHLQERQQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQQLLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTCAK 140

LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPPVQADLDAFHSGFQTCAK 140

EVLYQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA 207

EVLYQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDPREKGGAGASRVTIKQEPPGEDS-P 275

SGP-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A--V--KQEPPG-DSSP 249

APKRMKLDNRGGGSGGGPGGGAAAAAALLGPDAAAAALLRPDAALLSSLVAFGGGGGAPFPQAAAAA 345

APKRPKLEARG-----ALLGPEPA-LL-G-SLVAL-GGGAPFAQPA-- 288

PFCLPFCFLSPSAAAAYVQPFLLDKSGLEKLYPAAAAAPFLLYPGIPAPAAAAAFAFPCL 415

PFCLPFYLLSPSAAA-YVQPWLDKSGLDKLYPAAAA-PFLLYPGIPA-----AAAAAFAFPCL 348

SSVLSPPPEKAGA-AAATLLPHEVAPLGAP-HPQHPHGRTHLPFAGPREPGNPRESSAQEDPSQPGKEAP 482

SSVLSPPPEKAGATAGAPFLAHEVAPPG-PLRPQHAHSRTHLPRAV-----NPRESS-QEDATQPAKDAP 410

FIG. 3



hDEC2a

mDEC2a

SHARP-1

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTTLGHLEKAWLELTCLKHLKALTALTEQQHQKIIALONGERSLKSPIQSDLDAFHSGFQTCAG 140

LPEHLKLTTLGHLEKAWLELTCLKHLKALTALTEQQHQKIIALONGERSLKSPPVQADLDAFHSGFQTCAG 140

LPEHLKLTTLGHLEKAWLELTCLKHLKALTALTEQQHQKIIALONGERSLKSPPVQADLDAFHSGFQTCAG 140

EVLQYLSRFESWTPREPRCQVLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA 207

EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196

EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VT-PGRGPGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKKGAGASRVTIKQEPPEGDS-P 275

SGP-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A-V-KQEPGP-DSSP 249

SGS-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A-V-KQEPGP-DPSL 249

APKRMKLDNRGGGGGGGGGAAAAAALLGPDPAALLLRPDAALLSSLVAFGGGGGAPFPQAAAAA 345

APKRPKLEARG-----ALLGPEPA-LL-G-SLVAL-GGGAPFAQAAAA- 288

RPRG

253

PFCLPFCFLSPSAAAAYVQPFLLDKSGLEKYLPAAPAAAPFLLYPGIPAPAAAAAFAFPCL 415

PFCLPFYLLSPSAAA-YVQPWLDKSGLDKYLPAAPAAAPFLLYPGIPA-----AAAAAFAFPCL 348

SSVLSPPPEKAGA-AAATLLPHEVAPLGAP-HPQHHPGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 482

SSVLSPPPEKAGATAGAPFLAHEVAPPG-PLRPQHAHSRTHLPRAV-----NPESQ-QEDATQPAKDAP 410

FIG. 4